

SEQUENCE LISTING



5/a

(1) GENERAL INFORMATION:

(i) APPLICANT: Yoshinobu OKUNO et al.

(ii) TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

(B) STREET: 2033 K Street, N.W., #800

(C) CITY: Washington

(D) STATE: D.C.

(E) COUNTRY: U.S.A.

(F) ZIP: 20006

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: Wordperfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/918,568

(B) FILING DATE: August 1, 2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/004,422

(B) FILING DATE: January 8, 1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/443,862

(B) FILING DATE: May 22, 1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/229,781

(B) FILING DATE: April 19, 1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/054,016

(B) FILING DATE: April 29, 1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warren M. Cheek, Jr.

(B) REGISTRATION NUMBER: 33,367

(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-721-8200

(B) TELEFAX: 202-721-8250

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr Gly Leu Arg Asn

1 5

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (v) FRAGMENT TYPE: internal fragment
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:

- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
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 - (D) VOLUME:
 - (E) ISSUE:

- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys

1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:

- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
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 - (H) DOCUMENT NUMBER:

- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gly Met Arg Asn

1 5

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (v) FRAGMENT TYPE: internal fragment
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:

- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION: 9
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION: /note= "Val or Leu"
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Ile Asn Gly Lys Leu Asn Arg Xaa Ile Glu Lys

1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCAAAAGCA GGGGATAAT 19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT:
- (B) MAP POSITION:

- (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTAGAAACA AGGGTGTTTT T 21

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTTTTCGAG TACTGTGTCA ACA 23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:

- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCCCACTAC AATTGGGGAA ATG 23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:

- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTACAGAA ATTTGCTATG GCTG 24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:

- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:

- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTCCCCTAT TGTGACTGGG TGTA 24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:

- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTTATCATC ATCAGAATGA AC 22

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT:
- (B) MAP POSITION:
- (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
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 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTTCACCTT GTTTGTAATC CCGT 24

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCATTTTSTA CTCTTCCAT GCAT 24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
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- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCTACTCAA CTGTCGCCAG TTCA 24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT:
- (B) MAP POSITION:
- (C) UNITS:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:

- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTGTGTCGAC CTTCTCTGTG GAA 23

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:

- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:

- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTAGCATTG CCGGATGGCT 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:

- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATTATCCGGT TGCCAAAGGA TCG 23

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGAGCACTG GTAATCTGTT GCA 23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT:
- (B) MAP POSITION:

- (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:
 - (H) DOCUMENT NUMBER:
 - (I) FILING DATE:
 - (J) PUBLICATION DATE:
 - (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCATCAAATG CCTTTTGAGT GGA 23

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTAGAAGCT CAGCATTGTA TGT 23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:

- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATGCATTCA TCATCACATT TGTG 24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:

- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:

- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATACTTGGG ATAATCATAC GTC 23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCCATTTATG CTACAGTAGC AGG 23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCAGATTG AAGTGACTAA TGCT 24

(2) INFORMATION FOR SEO ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

~~(C) UNITS:~~

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATGCATCA CTCCAAATGG AAGC 24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTCCTGAA TTCTCCCTTC TAC 23

(2) INFORMATION FOR SEQ ID NO:27 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

~~(iv) ANTI-SENSE:~~

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Suita/1/89

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

~~(B) TITLE:~~

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGATAATAAA	TACAACCAAA	ATGAAAGCAA	AACTACTAGT	CCTGTTATGT	GCATTTACAG	60
CTACAGATGC	AGACACAATA	TGTATAGGCT	ACCATGCGAA	CAACTCAACC	GACACTGTTG	120
ACACAGTACT	TGAGAAGAAC	GTGACAGTGA	CACACTCTGT	CAACCTACTT	GAGGACAGTC	180
ACAACGGA	AACTATGTCGA	CTAAAAGGAA	TAGCCCCACT	ACAATTGGGT	AATTGCAGCA	240
TTGCCGGATG	GATCTTAGGA	AACCCAGAAT	GCGAATCACT	GTTTTCTAAG	GAATCATGGT	300
CCTACATTGC	AGAAACACCA	AACTCCGAGA	ATGGAACATG	TTACCCAGGG	TATTTGCGCG	360
ACTATGAGGA	ACTGAGGGAG	CAATTGAGTT	CAGTATCATC	ATTCGAGAGA	TTCGAAATAT	420
TCCCCAAAGA	AAGCTCATGG	CCCAACCACA	CCGTAACCAA	AGGAGTAACG	GCATCATGCT	480
CCCATAATGG	GAAAAGCAGT	TTTACAGAA	ATTTGCTATG	GCTGACGGGG	AAGAATGGCT	540
TGTACCCAAA	TCTGAGCAAG	TCCTATGTGA	ACAACAAAGA	GAAAGAAGTC	CTTGTACTAT	600
GGGGTGTTCA	TCACCCGTCT	AACATAGGGG	ACCAAAGGGC	CATCTATCAT	ACAGAAAATG	660
CTTATGTCTC	TGTAGTGTCT	TCACATTATA	GCAGGAGATT	CACCCCAGAA	ATAGCAAAAA	720

GACCCAAAGT AAGAGGTCAA GAAGGAAGAA TTAAGTACTA CTGGACTCTG CTGGAACCCG	780
GGGACACAAT AATATTTGAG GCAAATGGAA ATCTAATAGC GCCATGGTAT GCTTTCGCAC	840
TGAGTAGAGG CTTTGGGTCA GGAATCATCA CCTCAAACGC ATCAATGGAT GAATGTGACC	900
CGAAGTGTCA AACACCCCAG GGAGCTATAA ACAGTAGTCT TCCTTTCCAG AATGTACACC	960
CAGTCACAAT AGGAGAGTGT CCAAAGTATG TCAGGAGTAC AAAATTAAGG ATGGTTACAG	1020
GAATAAGGAA CATCCCATCC ATTCAATCCA GAGGTTTGTG TGGAGCCATT GCCGGTTTCA	1080
TTGAAGGGGG GTGGACTGGA ATGATAGATG GATGGTATGG TTATCATCAT CAGAATGAAC	1140
AAGGATCTGG CTATGCTGCG GATCAAAAAA GCACACAAAA TGCCATTAAC GGAATTACAA	1200
ACAAGGTGAA TTCTGTAATC GAGAAAATGA ACACTCAATT CACAGCTGTG GGCAAAGAAT	1260
TCAACAAATT AGAAAGAAGG ATGGAATACT TAAATAAAAA AGTTGATGAT GGATTTCTGG	1320
ACATTTGGAC ATATAATGCA GAATTGTTGG TTCTACTGGA AAATGAAAGG ACTTTGGATT	1380
TTCATGACTC AAATGTGAAG AATCTGTATG AGAAAGTAAA AAGCCAATTA AAGAATAATG	1440
CCAAAGAAAT AGGATACGGG TGTTTTGAAT TCTACCACAA GTGTAACAAT GAATGCATGG	1500
AAAGTGTGAA AAATGGAAC TATGACTATC CAAAATATTC CGAGGAATCA AAGTTAAACA	1560
GGGAAAAAAT TGATGGAGTG AAATTGGAAT CAATGGGAGT CTATCAGATT CTGGCGATCT	1620
ACTCAACTGT CGCCAGTTCA CTGGTGCTTT TGGTCTCCCT GGGGGCAATC AGCTTCTGGA	1680
TGTGTTCTAA TGGGTCTTTG CAGTGTAGAA TATGCATCTG AGACCAGAAT TTCAGAAATA	1740
TAAGAAAAAA CACC	1754

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/lzumi/5/65

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATAGACAACC	AAAAGCATAA	CAATGGCCAT	CATCTATCTC	ATACTCCTGT	TCACAGCAGT	60
GAGGGGGGAC	CAGATATGCA	TTGGATACCA	TGCCAATAAT	TCCACAGAAA	AGGTCGACAC	120
AATTCTAGAG	CGGAATGTCA	CTGTGACTCA	TGCCAAGGAC	ATCCTTGAGA	AGACCCACAA	180
CGGAAAGCTA	TGCAAACTAA	ACGGAATCCC	TCCACTTGAA	CTAGGGGACT	GTAGCATTGC	240
CGGATGGCTC	CTTGGAATC	CAGAATGTGA	TAGGCTTCTA	AGGGTGCCAG	AATGGTCCTA	300
TATAATGGAG	AAAGAAAACC	CGAGATACAG	TTTATGTTAC	CCAGGCAACT	TCAATGACTA	360
TGAAGAATTG	AAACATCTCC	TCAGCAGCGT	AAAACATTTT	GAGAAAGTAA	AGATTCTGCC	420
CAAAGATAGA	TGGACACAGC	ATACAACAAC	TGGAGGTTCA	AAGGCCTGCG	CAGTGTCAGG	480
TAAACCATCA	TTCTTCAGGA	ACATGGTCTG	GCTGACAAAG	AAAGGACCAA	ATTATCCGGT	540
TGCCAAAGGA	TCGTACAACA	ATACGAGCGG	AGAGCAAATG	CTAATAATTT	GGGGAGTGCA	600
CCATCCTAAT	GATGAGGCAG	AACAAAGAGC	ATTGTACCAG	GAAGTGGGAA	CCTATGTTTC	660
CGCAAGCACA	TCAACATTGA	ACAAAAGGTC	AATCCCTGAA	ATAGCAGCAA	GGCCTAAAGT	720
GAATGGACTA	GGAAGTAGAA	TGGAATTCTC	TTGGACCCTC	TTGGATGTGT	GGGACACCAT	780

AAATTTTGAG AGCACTGGTA ATCTAGTTGC ACCAGAGTAT GGATTCAAAA TATCGAAAAG	840
AGGTAGTTCA GGGATCATGA AGACAGAAGG AACACTTGGG AACTGTGAGA CCAAATGCCA	900
AACTCCTTTG GCAGCAATAA ATACAACACT ACCTTTTCAC AATGTCACCC CACTGACAAT	960
AGGTGAATGC CCCAAATATG TAAAATCGGA GAAATTGGTC TTAGCAACAG GACTAAGGAA	1020
TGTTCCCCAG ATTGAATCAA GAGGATTGTT TGGGGCAATA GCTGGCTTTA TAGAAGGAGG	1080
ATGGCAAGGA ATGGTTGATG GTTGGTATGG ATACCATCAC AGCAATGACC AGGGATCAGG	1140
GTATGCAGCA GACAAAGAAT CCACTCAAAA GGCATTTGAT GGAATCACCA ACAAGGTAAA	1200
TTCTGTGATT GAAAAGATGA ACACCCAATT TGAAGCTGTT GGGAAAGAAT TCAATAATTT	1260
AGAGAAAAGA CTGGAGAACT TGAACAAAAA GATGGAAGAC GGGTTTCTAG ATGTGTGGAC	1320
ATACAATGCT GAGCTTCTAG TTCTGATGGA AAATGAGAGG ACACTTGACT TCCATGATTC	1380
TAATGTCAAG AACCTGTATG ATAAAGTCAG AATGCAGCTG AGAGACAACG TCAAAGAACT	1440
AGGAAATGGA TGTTTTGAAT TTTATCACAA ATGTGACGAT GAATGCATGA ATAGTGTGAA	1500
AAACGGGACG TATGATTATC CCAAGTATGA AGAAGAATCT AACTTAAATA GAAATGAAAT	1560
CAAAGGGGTA AAATTGAGCA GCATGGGGGT TTACCAAATT CTTGCCATTT ATGCTACAGT	1620
TGCAGGTTCT CTGTCACTGG CAATCATGAT GGCTGGGATC TCTTTCTGGA TGTGCTCCAA	1680
CGGGTCTCTG CAGTGCAGAA TCTGCATATG ATTGTAATTT ATTTTATA	1728

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/PR/8/34

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTTTCCAGA ATATACACCC AGTCACAATA GGAGAGTGCC CAAAATACGT CAGGAGTGCC	60
AAATTGAGGA TGGTTACAGG ACTAAGGAAC ATCCCGTCCA TTCAATCCAG AGGTCTATTT	120
GGAGCCATTG CCGGTTTTAT TGAAGGGGGA TGGACTGGAA TGATAGATGG ATGGTATGGT	180
TATCATCATC AGAATGAACA GGGATCAGGC TATGCAGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAC TCTGTTATCG AGAAAATGAA CACTCAATTC	300
ACAGCTGTGG GTAAAGAATT CAACAAATTA GAAAAAGGA TGGAAAATTT AAATAAAAAA	360
GTTGATGATG GATTCTGGA CATTTGGACA TATAATGCAG AATTGTTAGT TCTACTGGAA	420
AATGAAAGGA CTCTGGATTT CC	442

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Bangkok/10/83

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

~~(B) TITLE:~~

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTACGT CAGGAGTACA	60
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGTTT	120
GGAGCCATTG CCGGTTTCAT TGAAGGGGGA TGGACTGGAA TGATAGATGG ATGGTATCGT	180
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAC TCTGTAATCG AGAAAATGAA CACTCAATTC	300
ACAGCTGTGG GTAAAGAATT CAACAAATTA GAAAAAGGA TGGAAAACCTT AAATAAAAAA	360
GTTGATGATG GATTCTGGA CATTGGACA TATAATGCAG AATTGTTGGT TCTACTGGAA	420
AATG	424

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
~~(D) TOPOLOGY: linear~~

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Yamagata/120/86

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

~~(D) OTHER INFORMATION:~~

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTATGT CAGGAGTACA	60
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGTTT	120
GGAGCCATTG CCGGTTTCAT TGAAGGGGGG TGGACTGGAA TGATAGATGG ATGGTATGGT	180
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAT TCTGTAATCG AGAAAATGAA CACTCAATTC	300
ACAGCTGTGG GCAAAGAATT CAACAAATTA GAAAGAAGGA TGGAAAACCTT AAATAAAAAA	360
GTTGATGATG GATTCTGGA CATTTGGACA TATAATGCAG AATTGTTGGT CCTACTGGAA	420
AATG	424

(2) INFORMATION FOR SEQ ID NO:32:

~~(i) SEQUENCE CHARACTERISTICS:~~

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Osaka/930/88

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

~~(ix)~~ FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTATGT CAGGAGTACA	60
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGTTT	120
GGAGCCATTG CCGGTTTCAT AGAAGGGGGG TGGACTGGAA TGATAGATGG ATGGTATGGT	180
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GAATTACAAA CAAGGTGAAT TCTGTAATCG AGAAAATGAA CACTCAATTC	300

ACAGCTGTGG GCAAAGAATT CAACAAATTA GAAAGAAGGA TGGAAAACCTT AAATAAAAAA	360
GTTGATGATG GATTTCTGGA CATTTGGACA TATAATGCAG AATTGTTGGT TCTACTGGAA	420
AATGAAAGG	429

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: A/Okuda/57
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCAATAAATA CAACATTACC TTTTCACAAT GTCCACCCAC TGACAATAGG TGAGTGCCCC	60
AAATATGTAA AATCGGAGAA GTTGGTCTTA GCAACAGGAC TAAGGAATGT TCCCCAGATT	120

GAATCAAGAG GATTGTTTGG GGCAATAGCT GGTTTTATAG AAGGAGGATG GCAAGGAATG	180
GTTGACGGTT GGTATGGATA CCATCACAGC AATGACCAGG GATCAGGGTA TGCAGCAGAC	240
AAAGAATCGA CTCAAAAGGC ATTTGATGGA ATCAGCAACA AGCTAAATTC TCTGATTCAA	300
AAGATAACA CCCAATTGTA AGCTGTTGGG AAAGAATTCG GTAACCTAGA GAAAAGACTG	360
GAGAACTTGA ACAAAAAGAT GGAAGACGGG TTTCTAGATG	400

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: A/Adachi/2/57
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGCCTTGGAG CAATAAATAC AACATTGCCT TTTCACAATG TCCACCCACT GACAATAGGT	60
GAGTGCCCCA AATATGTAAA ATCGGAGAAG TTGGTCTTAG CAACAGGACT AAGGAATGTT	120
CCCCAGATTG AATCAAGAGG ATTGTTTGGG GCAATAGCTG GTTTTATAGA AGCAGGATCG	180
<hr/>	
CAAGGAATGG TTGATGGTTG GTATGGATAC CATCACAGCA ATGACCAGGG ATCAGGGTAT	240
GCAGCAGACA AAGAATCCAC TCAAAGGCA TTTGATGGAA TCACCAACAA GGTAAATTCT	300
GTGATTGAAA AGATGAACAC CCAATTTGAA GCTGTTGGGA AAGAATTCGG TAACTTAGAG	360
AGAAGACTGG AGAACTTGAA CAAAAGATG GAAGACGGGT TTCTAGATG	409

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: A/Kumamoto/1/65
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

~~(vii) IMMEDIATE SOURCE:~~

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:~~

CTCCTTTGGA GCAATAAATA CAACATTACC TTTTCACAAT GTCCACCCAC TGACAATAGG	60
TGAATGCCCC AAATATGTAA AATCGGAGAA ACTGGTCTTA GCAACAGGAC TAAGGAATGT	120
TCCCCAGATT GAATCAAGAG GATTGTTTGG GGCAATAGCT GGCTTTGTAG AAGGAGGATG	180
GCAAGGAATG ATTGATGGTT GGTATGGATA CCATCACAGC AATGATCAGG GATCAGGGTT	240
TGCAGCAGAC AAAGAATCCA CTCAAAGGC ATTTGATGGA ATCACCAACA AGGTAAATTC	300
TGTGATTGAA AAGATGAACA CCCAATTTGA AGCTGTTGGG AAAGAATTCA ATAATTTAGA	360
GAAAAGACTG GAGAACTTGA ACAAAGGAT GGAAGACGGG TTTCTAGATG	410

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Kaizuka/2/65

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

- (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
-
- (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
- (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
- (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AATACAACAC TACCTTTTCA CAATGTCCAC CCACTGACAA TAGGTGAATG CCCCAAATAT	60
GTAAAATCGG AGAAATTGGT CTTAGCAACA GGACTAAGGA ATGTTCCCCA GATTGAATCA	120
AGAGGATTGT TTGGGGCAAT AGCTGGCTTT ATAGAAGGAG GATGGCAAGG AATGGTTGAT	180
GGTTGGTATG GATACCATCA CAGCAATGAC CAGGGATCAG GGTATGCAGC AGACAAAGAA	240
TCCACTCAAA AGGCATTTGA TGAATCACC AACAAAGTAA ATTCTGTGAT TGAAAAGATG	300
AACACCCAAT TTGAAGCTGT TGGGAAAGAA TTCAATAATT TAGAGAAAAG ACTGGAGAAC	360
TTGAACAAAA AGATGGAAGA CGGGTTTCTA GATG	394

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A2/Aichi/2/68

- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- ~~(D) DEVELOPMENTAL STAGE:~~
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:

(F) PAGES:

(G) DATE:

~~(H) DOCUMENT NUMBER:~~

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGACAAGCC CTTTCAAAAC GTAAACAAGA TCACATATGG AGCATGCCCC AAGTATGTTA	60
AGCAAAACAC CCTGAAGTTG GCAACAGGGA TGCGBAATGT ACCAGAGAAA CAAACTAGAG	120
GCCTATTCGG CGCAATAGCA GGTTCATAG AAAATGGTTG GGAGGGAATG ATAGACGGTT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTTAAAAGCA	240
CTCAAGCAGC CATCGACCAA ATCAATGGGA AATTGAACAG GGTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAATCGAA AAGGAATTC	329

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: A/Fukuoka/C29/85
- (B) STRAIN:
- ~~(C) INDIVIDUAL ISOLATE:~~
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGACAAACC CTTTCAAAAT GTAAACAAGA TCACATATGG GGCATGTCCC AGGTATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGCGBAATGT ACCAGAGAAA CAAACTAGAG	120
GCATATTCGG CGCAATAGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTTAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAATCGAA AAGGAATTCT CAGA	334

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Sichuan/2/87

~~(B) STRAIN:~~

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGACAAACC CTTTCAAAT GTAAACAAGA TCACATATGG GGCATGTCCC AGATATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGCGGAATGT ACCAGAGAAA CAAACTAGAG	120
GCATATTCGG CGCAATAGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGCT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAACCGAA AAGGAATTC	329

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

~~(A) ORGANISM: A/Ibaraki/1/90~~

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGACAAACC CTTTCAAAAT ATAAACAGGA TCACATATGG GGCATGTCCC AGATATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGCGGAATGT ACCAGAGAAA CAAACTAGAG	120
GCATATTCGG CGCAATCGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTTAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAATCGAA AAGGAATTCT CAGA	334

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Suita/1/90

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGACAAACC CTTTCAAAAT GTAAACAGGA TCACATATGG GGCATGTCCC AGATATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGCGGAATGT ACCAGAAAAA CAAACTAGGG	120
GCATATTCGG CGCAATCGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT	180
GGTACGGTTT CAGGCATCAA AACTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAACCGAA AAGGAATTC	329

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTAGAAG CAAAAGCAGG GGTATACCA 30

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
-
- (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT:
- (B) MAP POSITION:
- (C) UNITS:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCTAGCAA AAGCAGGGGT TATACCATAG 30

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACAGATCTAG TAGAAACAAG GGTGTTTTT 29

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCTAGCAG AAACAAGGGT GTTTTAATT 30

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Okuda/57

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCTAGCAA AAGCAGGGGT TATACCATAG AAAACCAAAA GCAAAACA

48

ATG GCC ATC ATT TAT CTC ATT CTC CTG TTC ACA GCA GTG AGA GGG 93
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly

GAC CAG ATA TGC ATT GGA TAC CAT GCC AAT AAT TCC ACA GAG AAG 138
Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Lys

GTC GAC ACA ATT CTA GAG CGG AAC GTC ACT GTG ACT CAT GCC AAG 183
Val Asp Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys

GAC ATC CTT GAG AAG ACC CAT AAC GGA AAG TTA TGC AAA CTA AAC 228
Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn

GGA ATC CCT CCA CTT GAA CTA GGG GAC TGT AGC ATT GCC GGA TGG 273
Gly Ile Pro Pro Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp

CTC CTT GGA AAT CCA AAA TGT GAT AGG CTT CTA AGT GTG CCA GAA 318
Leu Leu Gly Asn Pro Lys Cys Asp Arg Leu Leu Ser Val Pro Glu

CGG TCC TAT ATA TTG GAG AAA GAA AAC CCG AGA GAC GGT TTG TGT 363
Arg Ser Tyr Ile Leu Glu Lys Glu Asn Pro Arg Asp Gly Leu Cys

TAT CCA GGC AGC TTC AAT GAT TAT GAA GAA TTG AAA CAT CTC CTC 408

Tyr Pro Gly Ser Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu

AGC AGC GTG AAA CAT TTC GAG AAA GTA AAG ATT CTG CCC AAA GAT 453
Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu Pro Lys Asp

110	115	120	
AGA TGG ACA CAG CAT ACA ACA ACT GGA GGT TCA CGG GCC TGC GCG			498
Arg Trp Thr Gln His Thr Thr Thr Gly Gly Ser Arg Ala Cys Ala			
125	130	135	
GTG TCT GGT AAT CCA TCA TTT TTC AGG AAC ATG GTC TGG CTG ACA			543
Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu Thr			
140	145	150	
AAG GAA GGA TCA GAT TAT CCG GTT GCC AAA GGA TCG TAC AAC AAT			588
Lys Glu Gly Ser Asp Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn			
155	160	165	
ACA AGC GGA GAA CAA ATG CTA ATA ATT TGG GGG GTG CAC CAT CCC			633
Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val His His Pro			
170	175	180	
ATT GAT GAG ACA GAA CAA AGA ACA TTG TAC CAG AAT GTG GGA ACC			678
Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr			
185	190	195	
TAT GTT TCC GTA GGC ACA TCA ACA TTG AAC AAA AGG TCA ACC CCA			723
Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro			
200	205	210	
GAA ATA GCA ACA AGG CCT AAA GTG AAT GGA CAA GGA GGT AGA ATG			768
Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Gly Gly Arg Met			
215	220	225	
GAA TTC TCT TGG ACC CTC TTG GAT ATG TGG GAC ACC ATA AAT TTT			813
Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe			
230	235	240	
GAG AGT ACT GGT AAT CTA ATT GCA CCA GAG TAT GGA TTC AAA ATA			858

Glu Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile	
245	250 255
TCG AAA AGA GGT AGT TCA GGG ATC ATG AAA ACA GAA GGA ACA CTT	903
Ser Lys Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu	
260	265 270
GAG AAC TGT GAG ACC AAA TGC CAA ACT CCT TTG GGA GCA ATA AAT	948
Glu Asn Cys Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn	
275	280 285
ACA ACA TTA CCT TTT CAC AAT GTC CAC CCA CTG ACA ATA GGT GAG	993
Thr Thr Leu Pro Phe His Asn Val His Pro Leu Thr Ile Gly Glu	
290	295 300
TGC CCC AAA TAT GTA AAA TCG GAG AAG TTG GTC TTA GCA ACA GGA	1038
Cys Pro Lys Tyr Val Lys Ser Glu Lys Leu Val Leu Ala Thr Gly	
305	310 315
CTA AGG AAT GTT CCC CAG ATT GAA TCA AGA GGA TTG TTT GGG GCA	1083
Leu Arg Asn Val Pro Gln Ile Glu Ser Arg Gly Leu Phe Gly Ala	
320	325 330
ATA GCT GGT TTT ATA GAA GGA GGA TGG CAA GGA ATG GTT GAC GGT	1128
Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly	
335	330 345
TGG TAT GGA TAC CAT CAC AGC AAT GAC CAG GGA TCA GGG TAT GCA	1173
Trp Tyr Gly Tyr His His Ser Asn Asp Gln Gly Ser Gly Tyr Ala	
350	355 360
GCA GAC AAA GAA TCC ACT CAA AAG GCA TTT GAT GGA ATC ACC AAC	1218
Ala Asp Lys Glu Ser Thr Gln Lys Ala Phe Asp Gly Ile Thr Asn	
365	370 375

AAG GTA AAT TCT GTG ATT GAA AAG ATA AAC ACC CAA TTT GAA GCT	1263
Lys Val Asn Ser Val Ile Glu Lys Ile Asn Thr Gln Phe Glu Ala	
380 385 390	
<hr/>	
GTT GGG AAA GAA TTC GGT AAC TTA GAG AAA AGA CTG GAG AAC TTG	1308
Val Gly Lys Glu Phe Gly Asn Leu Glu Lys Arg Leu Glu Asn Leu	
395 400 405	
AAC AAA AAG ATG GAA GAC GGG TTT CTA GAT GTG TGG ACA TAC AAT	1353
Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn	
410 415 420	
GCT GAG CTT TTA GTT CTG ATG GAA AAT GAG AGG ACA CTT GAC TTT	1398
Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe	
425 430 435	
CAT GAT TCT AAT GTC AAG AAT CTG TAT AGT AAA GTC AGA ATG CAG	1443
His Asp Ser Asn Val Lys Asn Leu Tyr Ser Lys Val Arg Met Gln	
440 445 450	
CTG AGA GAC AAC GTC AAA GAA CTA GGA AAT GGA TGT TTT GAA TTT	1488
Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe	
455 460 465	
TAT CAC AAA TGT GAT GAT GAA TGC ATG AAT AGT GTG AAA AAC GGG	1533
Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly	
470 475 480	
ACA TAT GAT TAT CCC AAG TAT GAA GAA GAG TCT AAA CTA AAT AGA	1578
Thr Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg	
495 500 505	
AAT GAA ATC AAA GGG GTA AAA TTG AGC AGC ATG GGG GTT TAT CAA	1623
Asn Glu Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Tyr Gln	

510	515	520	
ATC CTT GCC ATT TAT GCT ACA GTA GCA GGT TCT ATG TCA CTG GCA			1668
Ile Leu Ala Ile Tyr Ala Thr Val Ala Gly Ser Met Ser Leu Ala			
525	530	535	
ATC ATG ATG GCT GGG ATC TCT TTC TGG GTG TGC TCC AAC GGG TCT			1713
Ile Met Met Ala Gly Ile Ser Phe Trp Val Cys Ser Asn Gly Ser			
540	545	550	
CTG CAG TGC AGG ATC TGC ATA TGATTATAAG TCATTTTATA ATTAAAAACA			1764
Leu Gln Cys Arg Ile Cys Ile			
555			
CCCTTGTTTC TGCTAGCCG			1783

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:

- (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
-
- (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
- (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
- (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS:
 - (B) TITLE:
 - (C) JOURNAL:
 - (D) VOLUME:
 - (E) ISSUE:
 - (F) PAGES:
 - (G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCCGTTTAGT TTGCATAACT TTCCG 25

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCCGGGATCA TGAAAACAGA AGGAAC 26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A/Okuda/57

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGCAAAAG CAGGGGTTAT ACCATAGAAA ACCAAAAGCA AAACAATGGC CATCATTTAT 60
CTCATTTCTCC TGTTACAGC AGTGAGAGGG GACCAGATAT GCATTGGATA CCATGCCAAT 120

AATTCCACAG	AGAAGGTCGA	CACAATTCTA	GAGCGGAACG	TCACTGTGAC	TCATGCCAAG	180
GACATCCTTG	AGAAGACCCA	TAACGGAAAG	TTATGCAAAC	TAAACGGATC	CGGGATCATG	240
AAAACAGAAG	GAACACTTGA	GAAGTGTGAG	ACCAAATGCC	AAACTCCTTT	GGCAGCAATA	300
<hr/>						
AATACAACAT	TACCTTTTCA	CAATGTCCAC	CCACTGACAA	TAGGTGAGTG	CCCCAAATAT	360
GTAAAATCGG	AGAAGTTGGT	CTTAGCAACA	GGACTAAGGA	ATGTTCCCCA	GATTGAATCA	420
AGAGGATTGT	TTGGGGCAAT	AGCTGGTTTT	ATAGAAGGAG	GATGGCAAGG	AATGGTTGAC	480
GGTTGGTATG	GATACCATCA	CAGCAATGAC	CAGGGATCAG	GGTATGCAGC	AGACAAAGAA	540
TCCACTCAAA	AGGCATTTGA	TGGAATCACC	AACAAGGTAA	ATTCTGTGAT	TGAAAAGATA	600
AACACCCAAT	TTGAAGCTGT	TGGGAAAGAA	TTCGGTAACT	TAGAGAAAAG	ACTGGAGAAC	660
TTGAACAAAA	AGATGGAAGA	CGGGTTTCTA	GATGTGTGGA	CATACAATGC	TGAGCTTTTA	720
GTTCTGATGG	AAAATGAGAG	GACACTTGAC	TTTCATGATT	CTAATGTCAA	GAATCTGTAT	780
AGTAAAGTCA	GAATGCAGCT	GAGAGACAAC	GTCAAAGAAC	TAGGAAATGG	ATGTTTTGAA	840
TTTTATCACA	AATGTGATGA	TGAATGCATG	AATAGTGTGA	AAAACGGGAC	ATATGATTAT	900
CCCAAGTATG	AAGAAGAGTC	TAAACTAAAT	AGAAATGAAA	TCAAAGGGGT	AAAATTGAGC	960
AGCATGGGGG	TTTATCAAAT	CCTTGCCATT	TATGCTACAG	TAGCAGGTTC	TATGTCACTG	1020
GCAATCATGA	TGGCTGGGAT	CTCTTTCTGG	GTGTGCTCCA	ACGGGTCTCT	GCAGTGCAGG	1080
ATCTGCATAT	GATTATAAGT	CATTTTATAA	TTAAAAACAC	CCTTGTTTCT	GCTAG	1135

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly

-15

-10

-5

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Lys

1

5

10

15

Val Asp Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys

20

25

30

Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn

35

40

45

Gly Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu

50

55

60

Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro

65

70

75

Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr

80

85

90

Val Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val

95

100

105

Pro Gln Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe

110

115

120

Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr

125

130

135

His His Ser Asn Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu

140

145

150

Ser Thr Gln Lys Ala Phe Asp Gly Ile Thr Asn Lys Val Asn Ser

155

160

165

Val Ile Glu Lys Ile Asn Thr Gln Phe Glu Ala Val Gly Lys Glu

170

175

180

Phe Gly Asn Leu Glu Lys Arg Leu Glu Asn Leu Asn Lys Lys Met

185

190

195

Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu

200

205

210

Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn

215

220

225

Val Lys Asn Leu Tyr Ser Lys Val Arg Met Gln Leu Arg Asp Asn

230

235

240

Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys

245

250

255

Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr Tyr Asp Tyr

260

265

270

Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys

275

280

285

Gly	Val	Lys	Leu	Ser	Ser	Met	Gly	Val	Tyr	Gln	Ile	Leu	Ala	Ile
			290					295					300	
<hr/>														
Tyr	Ala	Thr	Val	Ala	Gly	Ser	Met	Ser	Leu	Ala	Ile	Met	Met	Ala
			305					310					315	
Gly	Ile	Ser	Phe	Trp	Val	Cys	Ser	Asn	Gly	Ser	Leu	Gln	Cys	Arg
			320					325					330	
Ile	Cys	Ile												

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCTAGAAG CAAAGCAGGG GATAATTCTA 30

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAGATCTAG TAGAAACAAG GGTGTTTTT 29

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGGCTAGCAG AAACAAGGGT GTTTTAAATT 30

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1777 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to genomic RNA
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: A2/Aichi/2/68
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCTAGAAG CAAAGCAGGG GATAATTCTA TTAATC	36
ATG AAG ACC ATC ATT GCT TTG AGC TAC ATT TTC TGT CTG GCT CTC	81
Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Ala Leu	
-15 -10 -5	
GGC CAA GAC CTT CCA GGA AAT GAC AAC AGC ACA GCA ACG CTG TGC	126
Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys	
1 5 10	
CTG GGA CAT CAT GCG GTG CCA AAC GGA ACA CTA GTG AAA ACA ATC	171
Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr Ile	
15 20 25	

ACA GAT GAT CAG ATT GAA GTG ACT AAT GCT ACT GAG CTA GTT CAG	216
Thr Asp Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln	
30 35 40	
AGC TCC TCA ACG GGG AAA ATA TGC AAC AAT CCT CAT CGA ATC CTT	261
Ser Ser Ser Thr Gly Lys Ile Cys Asn Asn Pro His Arg Ile Leu	
45 50 55	
GAT GGA ATA GAC TGC ACA CTG ATA GAT GCT CTA TTG GGG GAC CCT	306
Asp Gly Ile Asp Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro	
60 65 70	
CAT TGT GAT GTT TTT CAA AAT GAG ACA TGG GAC CTT TTC GTT GAA	351
His Cys Asp Val Phe Gln Asn Glu Thr Trp Asp Leu Phe Val Glu	
75 80 85	
CGC AGC AAA GCT TTC AGC AAC TGT TAC CCT TAT GAT GTG CCA GAT	396
Arg Ser Lys Ala Phe Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp	
90 95 100	
TAT GCC TCC CTT AGG TCA CTA GTT GCC TCG TCA GGC ACT CTG GAG	441
Tyr Ala Ser Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu	
105 110 115	
TTT ATC ACT GAG GGT TTC ACT TGG ACT GGG GTC ACT CAG AAT GGG	486
Phe Ile Thr Glu Gly Phe Thr Trp Thr Gly Val Thr Gln Asn Gly	
120 125 130	
GGA AGC AAT GCT TGC AAA AGG GGA CCT GGT AGC GGT TTT TTC AGT	531
Gly Ser Asn Ala Cys Lys Arg Gly Pro Gly Ser Gly Phe Phe Ser	
135 140 145	
AGA CTG AAC TGG TTG ACC AAA TCA GGA AGC ACA TAT CCA GTG CTG	576
Arg Leu Asn Trp Leu Thr Lys Ser Gly Ser Thr Tyr Pro Val Leu	

150	155	160	
AAC GTG ACT ATG CCA AAC AAT GAC AAT TTT GAC AAA CTA TAC ATT			621
Asn Val Thr Met Pro Asn Asn Asp Asn Phe Asp Lys Leu Tyr Ile			
165	170	175	
TGG GGG ATT CAC CAC CCG AGC ACG AAC CAA GAA CAA ACC AGC CTG			666
Trp Gly Ile His His Pro Ser Thr Asn Gln Glu Gln Thr Ser Leu			
180	185	190	
TAT GTT CAA GCA TCA GGG AGA GTC ACA GTC TCT ACC AGG AGA AGC			711
Tyr Val Gln Ala Ser Gly Arg Val Thr Val Ser Thr Arg Arg Ser			
195	200	205	
CAG CAA ACT ATA ATC CCG AAT ATC GGG TCC AGA CCC TGG GTA AGG			756
Gln Gln Thr Ile Ile Pro Asn Ile Gly Ser Arg Pro Trp Val Arg			
210	215	220	
GGT CTG TCT AGT AGA ATA AGC ATC TAT TGG ACA ATA GTT AAG CCG			801
Gly Leu Ser Ser Arg Ile Ser Ile Tyr Trp Thr Ile Val Lys Pro			
225	230	235	
GGA GAC GTA CTG GTA ATT AAT AGT AAT GGG AAC CTA ATC GCT CCT			846
Gly Asp Val Leu Val Ile Asn Ser Asn Gly Asn Leu Ile Ala Pro			
240	245	250	
CGG GGT TAT TTC AAA ATG CGC ACT GGG AAA AGC TCA ATA ATG AGG			891
Arg Gly Tyr Phe Lys Met Arg Thr Gly Lys Ser Ser Ile Met Arg			
255	260	265	
TCA GAT GCA CCT ATT GAT ACC TGT ATT TCT GAA TGC ATC ACT CCA			936
Ser Asp Ala Pro Ile Asp Thr Cys Ile Ser Glu Cys Ile Thr Pro			
270	275	280	
AAT GGA AGC ATT CCC AAT GAC AAG CCC TTT CAA AAC GTA AAC AAG			981

AACACCCTTG TTTCTGCTAG CCG

1777

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATTGTTGCAT ATTTTCCCCG 20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (B) STRAIN:
 - (C) INDIVIDUAL ISOLATE:
 - (D) DEVELOPMENTAL STAGE:
 - (E) HAPLOTYPE:
 - (F) TISSUE TYPE:
 - (G) CELL TYPE:
 - (H) CELL LINE:
 - (I) ORGANELLE:
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT:
 - (B) MAP POSITION:
 - (C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATTGATACCT GTATTTCTGA 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1110 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to genomic RNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: A2/Aichi/2/68

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

~~(A) AUTHORS:~~

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTAGAAGCAA AGCAGGGGAT AATTCTATTA ATCATGAAGA CCATCATTGC TTTGAGCTAC	60
ATTTTCTGTC TGGCTCTCGG CCAAGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG	120
TGCCTGGGAC ATCATGCGGT GCCAAACGGA AACTAGTGA AAACAATCAC AGATGATCAG	180
ATTGAAGTGA CTAATGCTAC TGAGCTAGTT CAGAGCTCCT CAACGGGGAA AATATGCAAC	240
AATATTGATA CCTGTATTTT TGAATGCATC ACTCCAAATG GAAGCATTCC CAATGACAAG	300
CCCTTTCAAA ACGTAAACAA GATCACATAT GGAGCATGCC CCAAGTATGT TAAGCAAAAC	360
ACCCTGAAGT TGGCAACAGG GATGCGGAAT GTACCAGAGA AACAACTAG AGGCCTATTC	420
GGCGCAATAG CAGGTTTCAT AGAAAATGGT TGGGAGGGAA TGATAGACGG TTGGTACGGT	480
TTCAGGCATC AAAATTCTGA GGGCACAGGA CAAGCAGCAG ATCTTAAAAG CACTCAAGCA	540
GCCATCGACC AAATCAATGG GAAATTGAAC AGGGTAATCG AGAAGACGAA CGAGAAATTC	600
CATCAAATCG AAAAGGAATT CTCAGAAGTA GAAGGGAGAA TTCAGGACCT CGAGAAATAC	660

GTTGAAGACA CTAAAATAGA TCTCTGGTCT TACAATGCGG AGCTTCTTGT CGCTCTGGAG	720
AATCAACATA CAATTGACCT GACTGACTCG GAAATGAACA AGCTGTTTGA AAAAACAAGG	780
AGGCAACTGA GCGAAAATCG TGAACAGATC GCGAATCGTT GCTTCAAAAT ATACCACAAA	840
TGTGACAACG CTTGCATAGA GTCAATCAGA AATGGTACTT ATGACCATGA TGTATACAGA	900
GACGAAGCAT TAAACAACCG GTTTCAGATC AAAGGTGTTG AACTGAAGTC TGGATACAAA	960
GACTGGATCC TGTGGATTTT CTTTGCCATA TCATGCTTTT TGCTTTGTGT TGTTTTGCTG	1020
GGGTTCATCA TGTGGGCCTG CCAGAGAGGC AACATTAGGT GCAACATTTG CATTTGAGTG	1080
TATTAGTAAT TAAAAACACC CTTGTTTCTG	1110

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

~~(I) ORGANELLE:~~

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Lys	Thr	Ile	Ile	Ala	Leu	Ser	Tyr	Ile	Phe	Cys	Leu	Ala	Leu
-15						-10					-5			
Gly	Gln	Asp	Leu	Pro	Gly	Asn	Asp	Asn	Ser	Thr	Ala	Thr	Leu	Cys
1					5					10				
Leu	Gly	His	His	Ala	Val	Pro	Asn	Gly	Thr	Leu	Val	Lys	Thr	Ile
15					20					25				
Thr	Asp	Asp	Gln	Ile	Glu	Val	Thr	Asn	Ala	Thr	Glu	Leu	Val	Gln
30					35					40				
Ser	Ser	Ser	Thr	Gly	Lys	Ile	Cys	Asn	Asn	Ile	Asp	Thr	Cys	Ile
45					50					55				
Ser	Glu	Cys	Ile	Thr	Pro	Asn	Gly	Ser	Ile	Pro	Asn	Asp	Lys	Pro
60					65					70				
Phe	Gln	Asn	Val	Asn	Lys	Ile	Thr	Tyr	Gly	Ala	Cys	Pro	Lys	Tyr
75					80					85				
Val	Lys	Gln	Asn	Thr	Leu	Lys	Leu	Ala	Thr	Gly	Met	Arg	Asn	Val
90					95					100				
Pro	Glu	Lys	Gln	Thr	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe
105					110					115				
Ile	Glu	Asn	Gly	Trp	Glu	Gly	Met	Ile	Asp	Gly	Trp	Tyr	Gly	Phe
120					125					130				
Arg	His	Gln	Asn	Ser	Glu	Gly	Thr	Gly	Gln	Ala	Ala	Asp	Leu	Lys
135					140					145				
Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile	Asn	Gly	Lys	Leu	Asn	Arg

150	155	160
Val Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu Lys Glu		
165	170	175
Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val		
180	185	190
Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu		
195	200	205
Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu		
210	215	220
Met Asn Lys Leu Phe Glu Lys Thr Arg Arg Gln Leu Arg Glu Asn		
225	230	235
Ala Glu Glu Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys		
240	245	250
Asp Asn Ala Cys Ile Glu Ser Ile Arg Asn Gly Thr Tyr Asp His		
255	260	265
Asp Val Tyr Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys		
270	275	280
Gly Val Glu Leu Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile		
285	290	295
Ser Phe Ala Ile Ser Cys Phe Leu Leu Cys Val Val Leu Leu Gly		
300	305	310
Phe Ile Met Trp Ala Cys Gln Arg Gly Asn Ile Arg Cys Asn Ile		
315	320	325
Cys Ile		
330		